

## F i g . 1

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5'   9      18      27      36      45      54
   ATG GAA ATT ATT TCA TCA AAA CTA TTC ATT TTA TTG ACT TTA GCC ACT TCA AGC
   ---
   Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr Ser Ser

      63      72      81      90      99      108
   TTG TTA ACA TCA AAC ATT TTT TGT GCA GAT GAA TTA GTG ATG TCC AAT CTT CAC
   ---
   Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met Ser Asn Leu His

      117      126      135      144      153      162
   AGC AAA GAA AAT TAT GAC AAA TAT TCT GAG CCT AGA GGA TAC CCA AAA GGG GAA
   ---
   Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg Gly Tyr Pro Lys Gly Glu

      171      180      189      198      207      216
   AGA AGC CTC AAT TTT GAG GAA TTA AAA GAT TGG GGA CCA AAA AAT GTT ATT AAG
   ---
   Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp Trp Gly Pro Lys Asn Val Ile Lys

      225      234      243      252      261      270
   ATG AGT ACA CCT GCA GTC AAT AAA ATG CCA CAC TCC TTC GCC AAC TTG CCA TTG
   ---
   Met Ser Thr Pro Ala Val Asn Lys Met Pro His Ser Phe Ala Asn Leu Pro Leu

      279      288      297      306      315      324
   AGA TTT GGG AGG AAC GTT CAA GAA GAA AGA AGT GCT GGA GCA ACA GCC AAC CTG
   ---
   Arg Phe Gly Arg Asn Val Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu

      333      342      351      360      369      378
   CCT CTG AGA TCT GGA AGA AAT ATG GAG GTG AGC CTC GTG AGA CGT GTT CCT AAC
   ---
   Pro Leu Arg Ser Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn

      387      396      405      414      423      432
   CTG CCC CAA AGG TTT GGG AGA ACA ACA ACA GCC AAA AGT GTC TGC AGG ATG CTG
   ---
   Leu Pro Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu

      441      450      459      468      477      486
   AGT GAT TTG TGT CAA GGA TCC ATG CAT TCA CCA TGT GCC AAT GAC TTA TTT TAC
   ---
   Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu Phe Tyr

      495      504      513      522      531      540
   TCC ATG ACC TGC CAG CAC CAA GAA ATC CAG AAT CCC GAT CAA AAA CAG TCA AGG
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   Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln Lys Gln Ser Arg

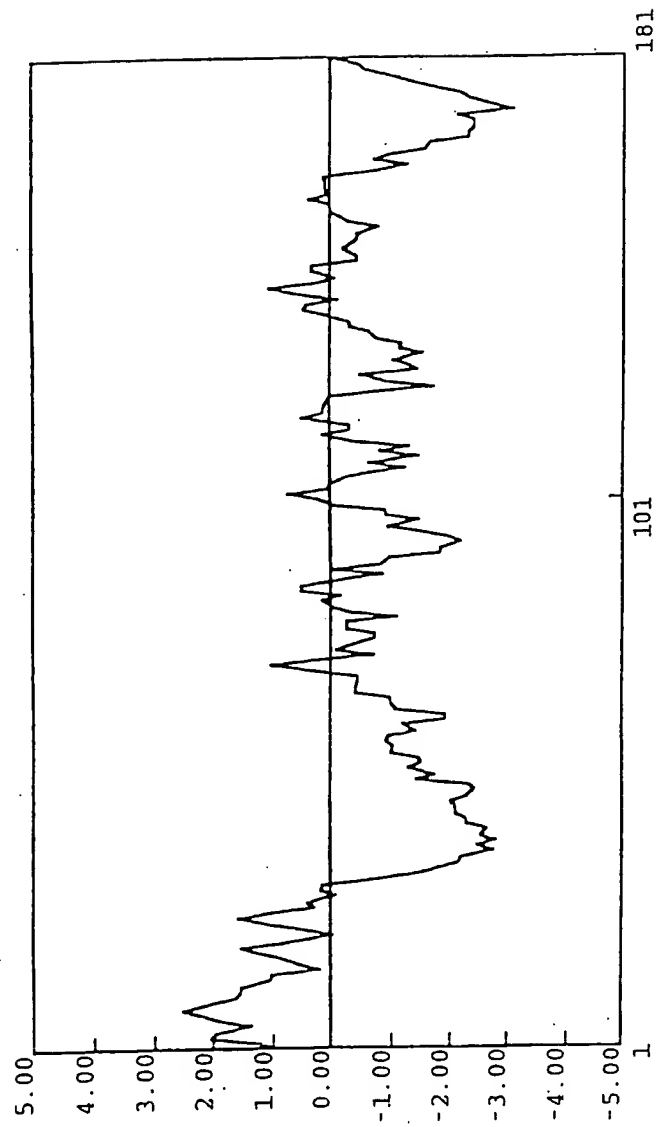
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TAA 3'

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2/9

F i g . 2



## F i g . 3

5	ATG	GAA	ATT	ATT	TCA	TCA	AAA	CTA	TTC	ATT	TTA	TTG	ACT	TTA	GCC	ACT	TCA	AGC	54
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Met	Glu	Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser	
	TTG	TTA	ACA	TCA	AAC	ATT	TTT	TGT	GCA	GAT	GAA	TTA	GTG	ATG	TCC	AAT	CTT	CAC	108
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	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Glu	Leu	Val	Met	Ser	Asn	Leu	His	
	AGC	AAA	GAA	AAT	TAT	GAC	AAA	TAT	TCT	GAG	CCT	AGA	GGA	TAC	CCA	AAA	GGG	GAA	162
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Tyr	Pro	Lys	Gly	Glu	
	AGA	AGC	CTC	AAT	TTT	GAG	GAA	TTA	AAA	GAT	TGG	GGA	CCA	AAA	AAT	GTT	ATT	AAG	216
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys	
	ATG	AGT	ACA	CCT	GCA	GTC	AAT	AAA	ATG	CCA	CAC	TCC	TTC	GCC	AAC	TTG	CCA	TTG	270
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys	Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu	
	AGA	TTT	GGG	AGG	AAC	GTT	CAA	GAA	GAA	AGA	AGT	GCT	GGA	GCA	ACA	GCC	AAC	CTG	324
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Arg	Phe	Gly	Arg	Asn	Val	Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu	
	CCT	CTG	AGA	TCT	GGA	AGA	AAT	ATG	GAG	GTG	AGC	CTC	GTG	AGA	CGT	GTT	CCT	AAC	378
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Pro	Leu	Arg	Ser	Gly	Arg	Asn	Met	Glu	Val	Ser	Leu	Val	Arg	Arg	Val	Pro	Asn	
	CTG	CCC	CAA	AGG	TTT	GGG	AGA	ACA	ACA	ACA	GCC	AAA	AGT	GTC	TGC	AGG	ATG	CTG	432
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu	
	AGT	GAT	TTG	TGT	CAA	GGA	TCC	ATG	CAT	TCA	CCA	TGT	GCC	AAT	GAC	TTA	TTT	TAC	486
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	Phe	Tyr	
	TCC	ATG	ACC	TGC	CAG	CAC	CAA	GAA	ATC	CAG	AAT	CCC	GAT	CAA	AAA	CAG	TCA	AGG	540
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	Gln	Lys	Gln	Ser	Arg	
	AGA	CTG	CTA	TTC	AAG	AAA	ATA	GAT	GAT	GCA	GAA	TTG	AAA	CAA	GAA	AAA	TAA	3'	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Arg	Leu	Leu	Phe	Lys	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***		

## F i g . 4

5'	ATG	GAA	ATT	ATT	TCA	TTA	AAA	CGA	TTC	ATT	TTA	TTG	ATG	TTA	GCC	ACT	TCA	AGC	54
	Met	Glu	Ile	Ile	Ser	Leu	Lys	Arg	Phe	Ile	Leu	Leu	Met	Leu	Ala	Thr	Ser	Ser	
	TTG	TTA	ACA	TCA	AAC	ATC	TTC	TGC	ACA	GAC	GAA	TCA	AGG	ATG	CCC	AAT	CTT	TAC	108
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	Glu	Ser	Arg	Met	Pro	Asn	Leu	Tyr	
	AGC	AAA	AAG	AAT	TAT	GAC	AAA	TAT	TCC	GAG	CCT	AGA	GGA	GAT	CTA	GGC	TGG	GAG	162
	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Asp	Leu	Gly	Trp	Glu	
	AAA	GAA	AGA	AGT	CTT	ACT	TTT	GAA	GAA	GTA	AAA	GAT	TGG	GCT	CCA	AAA	ATT	AAG	216
	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val	Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys	
	ATG	AAT	AAA	CCT	GTA	GTC	AAC	AAA	ATG	CCA	CCT	TCT	GCA	GCC	AAC	CTG	CCA	CTG	270
	Met	Asn	Lys	Pro	Val	Val	Asn	Lys	Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu	
	AGA	TTT	GGG	AGG	AAC	ATG	GAA	GAA	GAA	AGG	AGC	ACT	AGG	GCG	ATG	GCC	CAC	CTG	324
	Arg	Phe	Gly	Arg	Asn	Met	Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu	
	CCT	CTG	AGA	CTC	GGA	AAA	AAT	AGA	GAG	GAC	AGC	CTC	TCC	AGA	TGG	GTC	CCA	AAT	378
	Pro	Leu	Arg	Leu	Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn	
	CTG	CCC	CAG	AGG	TTT	GGA	AGA	ACA	ACA	GCC	AAA	AGC	ATT	ACC	AAG	ACC	CTG	432	
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu	
	AGT	AAT	TTG	CTC	CAG	CAG	TCC	ATG	CAT	TCA	CCA	TCT	ACC	AAT	GGG	CTA	CTC	TAC	486
	Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu	Leu	Tyr	
	TCC	ATG	GCC	TGC	CAG	CCC	CAA	GAA	ATC	CAG	AAT	CCT	GGT	CAA	AAG	AAC	CTA	AGG	540
	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln	Lys	Asn	Leu	Arg	
	AGA	CGG	GGA	TTC	CAG	AAA	ATA	GAT	GAT	GCA	GAA	TTG	AAA	CAA	GAA	AAA	TAA	3'	
	Arg	Arg	Gly	Phe	Gln	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***		

## F i g . 5

```

      9      18      27      36      45      54
5'  ATG GAA ATT ATT TCA TCA AAG CGA TTC ATT TTA TTG ACT TTA GCA ACT TCA AGC
    ---
    Met Glu Ile Ile Ser Ser Lys Arg Phe Ile Leu Leu Thr Leu Ala Thr Ser Ser

      63      72      81      90      99      108
    TTC TTA ACT TCA AAC ACC CTT TGT TCA GAT GAA TTA ATG ATG CCC CAT TTT CAC
    ---
    Phe Leu Thr Ser Asn Thr Leu Cys Ser Asp Glu Leu Met Met Pro His Phe His

      117      126      135      144      153      162
    AGC AAA GAA GGT TAT GGA AAA TAT TAC CAG CTG AGA GGA ATC CCA AAA GGG GTA
    ---
    Ser Lys Glu Gly Tyr Gly Lys Tyr Tyr Gln Leu Arg Gly Ile Pro Lys Gly Val

      171      180      189      198      207      216
    AAG GAA AGA AGT GTC ACT TTT CAA GAA CTC AAA GAT TGG GGG GCA AAG AAA GAT
    ---
    Lys Glu Arg Ser Val Thr Phe Gln Glu Leu Lys Asp Trp Gly Ala Lys Lys Asp

      225      234      243      252      261      270
    ATT AAG ATG AGT CCA GCC CCT GCC AAC AAA GTG CCC CAC TCA GCA GCC AAC CTT
    ---
    Ile Lys Met Ser Pro Ala Pro Ala Asn Lys Val Pro His Ser Ala Ala Asn Leu

      279      288      297      306      315      324
    CCC CTG AGG TTT GGG AGG AAC ATA GAA GAC AGA AGA AOC CCC AGG GCA CGG GCC
    ---
    Pro Leu Arg Phe Gly Arg Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala

      333      342      351      360      369      378
    AAC ATG GAG GCA GGG ACC ATG AGC CAT TTT CCC AGC CTG CCC CAA AGG TTT GGG
    ---
    Asn Met Glu Ala Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly

      387      396      405      414      423      432
    AGA ACA ACA GCC AGA CGC ATC ACC AAG ACA CTG GCT GGT TTG CCC CAG AAA TCC
    ---
    Arg Thr Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser

      441      450      459      468      477      486
    CTG CAC TCC CTG GCC TCC AGT GAA TCG CTC TAT GCC ATG ACC CGC CAG CAT CAA
    ---
    Leu His Ser Leu Ala Ser Ser Glu Ser Leu Tyr Ala Met Thr Arg Gln His Gln

      495      504      513      522      531      540
    GAA ATT CAG AGT CCT GGT CAA GAG CAA CCT AGG AAA CGG GTG TTC ACG GAA ACA
    ---
    Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val Phe Thr Glu Thr

      549      558      567      576      585      594
    GAT GAT GCA GAA AGG AAA CAA GAA AAA ATA GGA AAC CTC CAG CCA GTC CTT CAA
    ---
    Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn Leu Gln Pro Val Leu Gln

      603      612
    GGG GCT ATG AAG CTG TGA 3'
    ---
    Gly Ala Met Lys Leu ***

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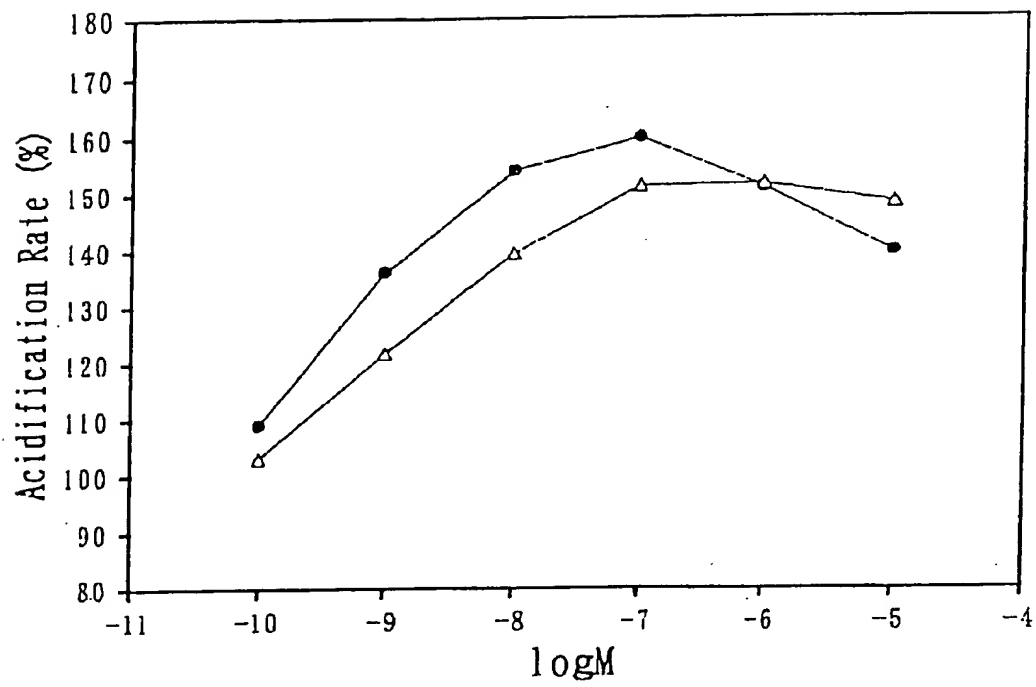
F i g . 6

hLPLRF.aa	1	MEIISKRFI	LLTLATSSLL	TSNIFCADEL	VMSNLHSEN	YDKYSEPRG	50
bLPLRF.aa	1	MEIISKRFI	LLTLATSSLL	TSNIFCADEL	RMPNLYSKN	YDKYSEPRGD	50
rLPLRF.aa	1	MEIISKRFI	LLTLATSSFL	TSNTLQSDLI	MPHFHSKEG	YKYYQLRGI	50
hLPLRF.aa	51	--YPKG	ER	SLNFEELKDW	GPKNVTKMST	PAVNKMPHSF	ANLPLRFGRN
bLPLRF.aa	51	LGWEK	ER	SLTFEEYKDW	APK--IKMKN	PAVNKMPHSA	ANLPLRFGRN
rLPLRF.aa	51	---PKGVER	SVTFQELKDW	GAKQIKMSP	APANKMPHSA	ANLPLRFGRN	100
hLPLRF.aa	101	VQEERSAGAT	ANLPLRSGRN	MEMSLMRRVP	NLPQRFGRIT	TAKSVCRMLS	150
bLPLRF.aa	101	MEEERSIRAM	HLPLRLGN	REDSLSRWVP	NLPQRFGRIT	TAKSITKILS	150
rLPLRF.aa	101	IEDRRSEPRAR	ANM-----	EAGTMSHFE	SLPQRFGRIT	ARRITKTIA	150
hLPLRF.aa	151	DLQCSMHSH	CANDLEYSMT	CQHQEIQNP	QKQSRRLIFK	KIDDAELKQE	200
bLPLRF.aa	151	NLQCSMHSH	STNGLLYSMA	CQHQEIQNP	QKNLRRRQFQ	KIDDAELKQE	200
rLPLRF.aa	151	GLPQKSTHSL	ASSESLYAMT	RQHQEIQSPG	QEQPRRMT	ETDDAERKQE	200
hLPLRF.aa	201	K*	-----	220	230	240	250
bLPLRF.aa	201	K*	-----	220	230	240	250
rLPLRF.aa	201	KIGNLQPVLO	GAMKL*	-----	220	240	250

## F i g . 7

1	TTTAGACTTAGACGAAATGGAAATTATTTTCATTAAAACGATTTCATTTTATTGACTGTG	58
1	MetGluIleIleSerLeuLysArgPheIleLeuLeuThrVal	14
59	GCAACTTCAAGCTTCTTAACATCAAACACCTTCTGTACAGATGAGTTCATGATGCCTCAT	118
15	AlaThrSerSerPheLeuThrSerAsnThrPheCysThrAspGluPheMetMetProHis	34
119	TTTCACAGCAAAGAAGGTGACGGAAAATACTCCCAGCTGAGAGGAATCCCAAAAGGGGAA	178
35	PheHisSerLysGluGlyAspGlyLysTyrSerGlnLeuArgGlyIleProLysGlyGlu	54
179	AAGGAAAGAAGTGTCAGTTTTCAAGAACTAAAAGATTGGGGGGCAAAGAATGTTATTAAG	238
55	LysGluArgSerValSerPheGlnGluLeuLysAspTrpGlyAlaLysAsnValIleLys	74
239	ATGAGTCCAGCCCCTGCCAACAAAGTGCCCCACTCAGCAGCCAACCTGCCCCCTGAGATTT	298
75	MetSerProAlaProAlaAsnLysValProHisSerAlaAlaAsnLeuProLeuArgPhe	94
299	GGAAGGACCATAGATGAGAAAAGAAGCCCCGCAGCACGGGTCAACATGGAGGCAGGGACC	358
95	GlyArgThrIleAspGluLysArgSerProAlaAlaArgValAsnMetGluAlaGlyThr	114
359	AGGAGCCATTTCCCCAGCCTGCCCCAAAGGTTTGGGAGAACAACAGCCAGAAGCCCCAAG	418
115	ArgSerHisPheProSerLeuProGlnArgPheGlyArgThrThrAlaArgSerProLys	134
419	ACACCCGCTGATTTGCCACAGAAACCCCTGCACTCACTGGGCTCCAGCGAGTTGCTCTAC	478
135	ThrProAlaAspLeuProGlnLysProLeuHisSerLeuGlySerSerGluLeuLeuTyr	154
479	GTCATGATCTGCCAGCACCAAGAAATTCAGAGTCCTGGTGGAAAGCGAACGAGGAGAGGA	538
155	ValMetIleCysGlnHisGlnGluIleGlnSerProGlyGlyLysArgThrArgArgGly	174
539	GCGTTTGTGGAAACAGATGATGCAGAAAGGAAACCAGAAAAATAGGAAACCTCGAGCCCCG	598
175	AlaPheValGluThrAspAspAlaGluArgLysProGluLys***	188
599	ACTTCAAGAGGCTACGGAGC	618
188		188

F i g . . 8



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F i g . 9

